

FIG. 1A

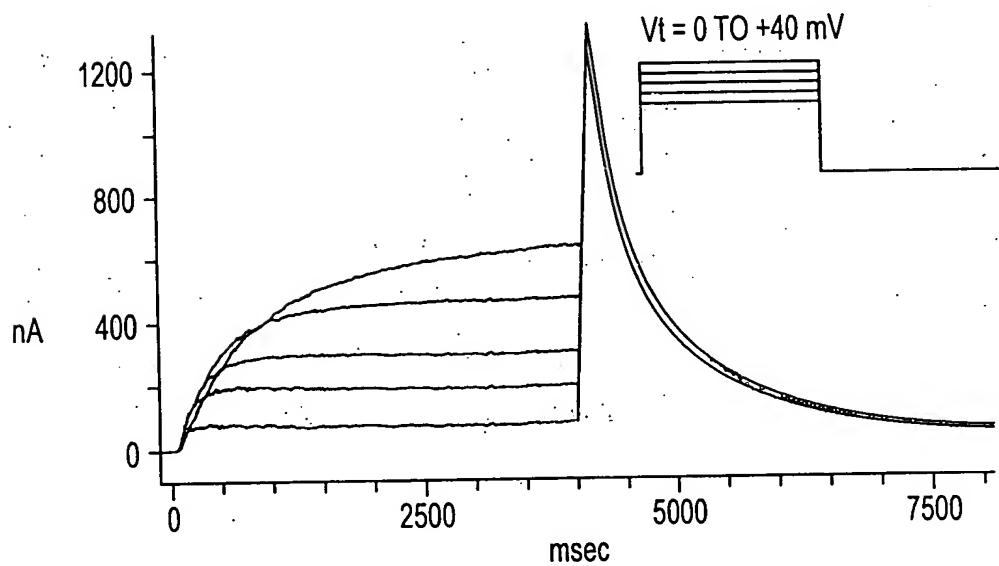


FIG. 1B

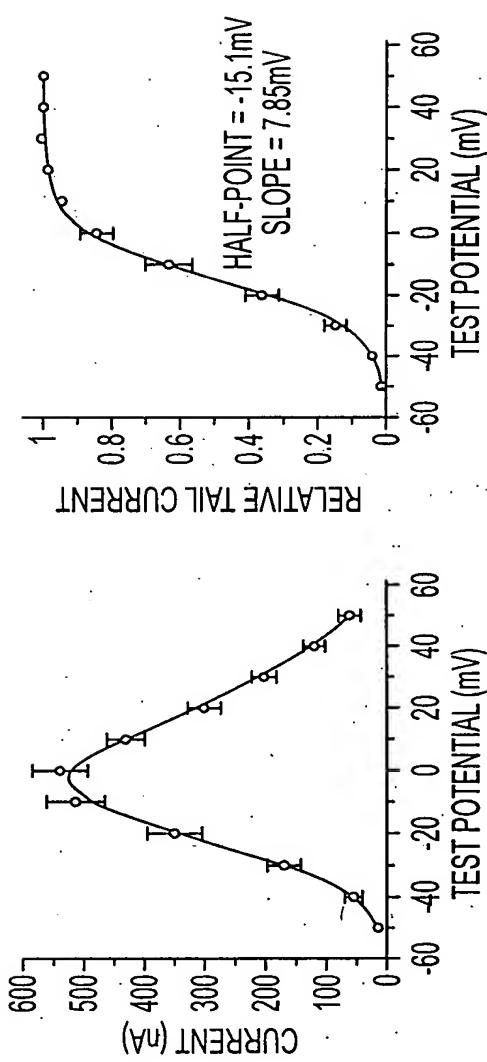


FIG. 1D

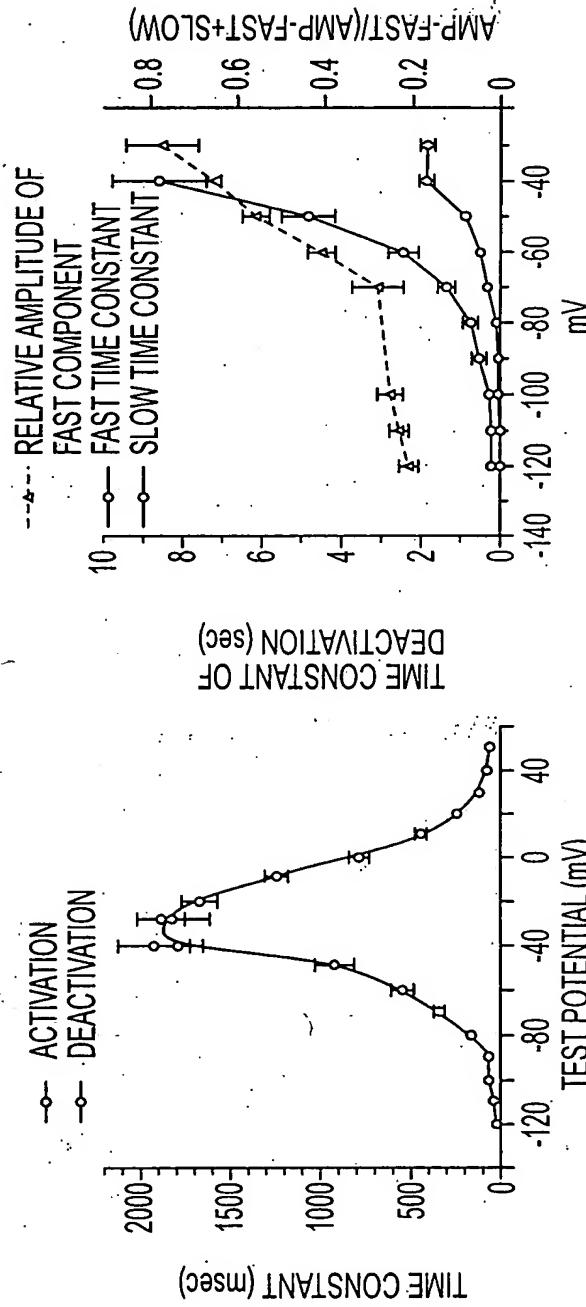
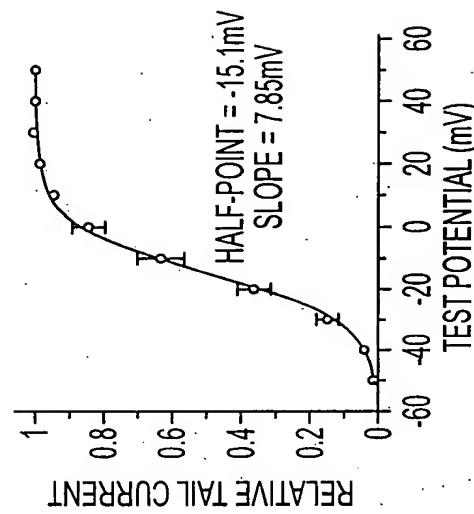


FIG. 2D

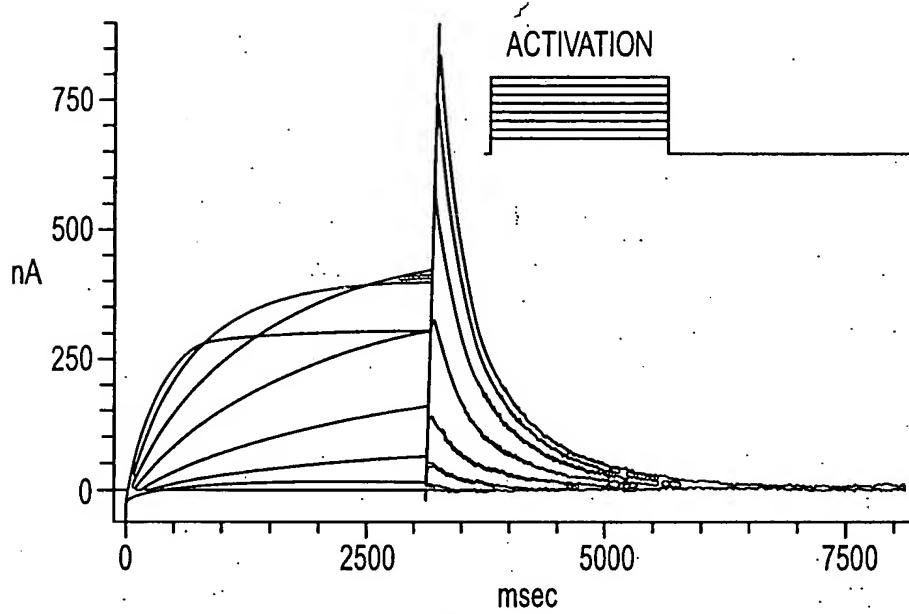


FIG. 2A

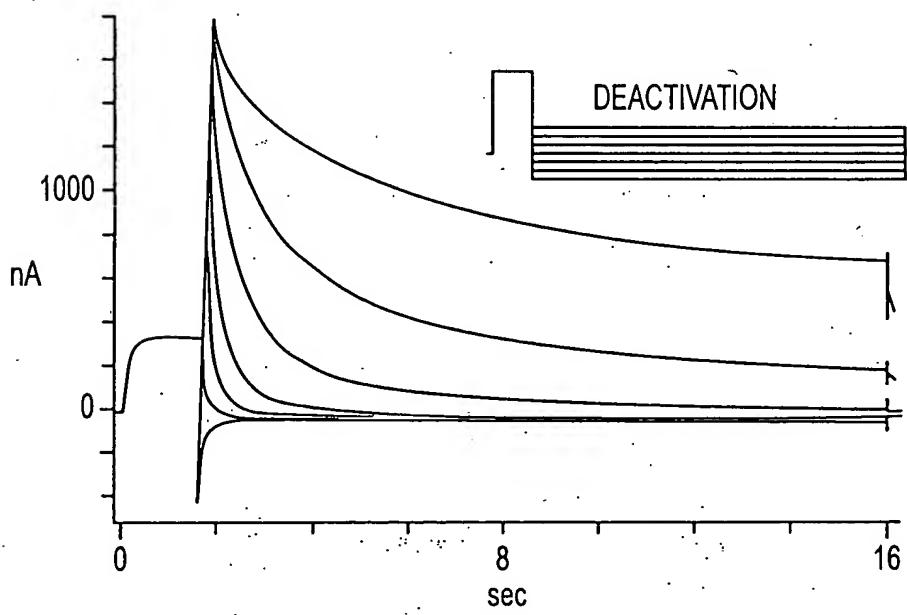


FIG. 2B

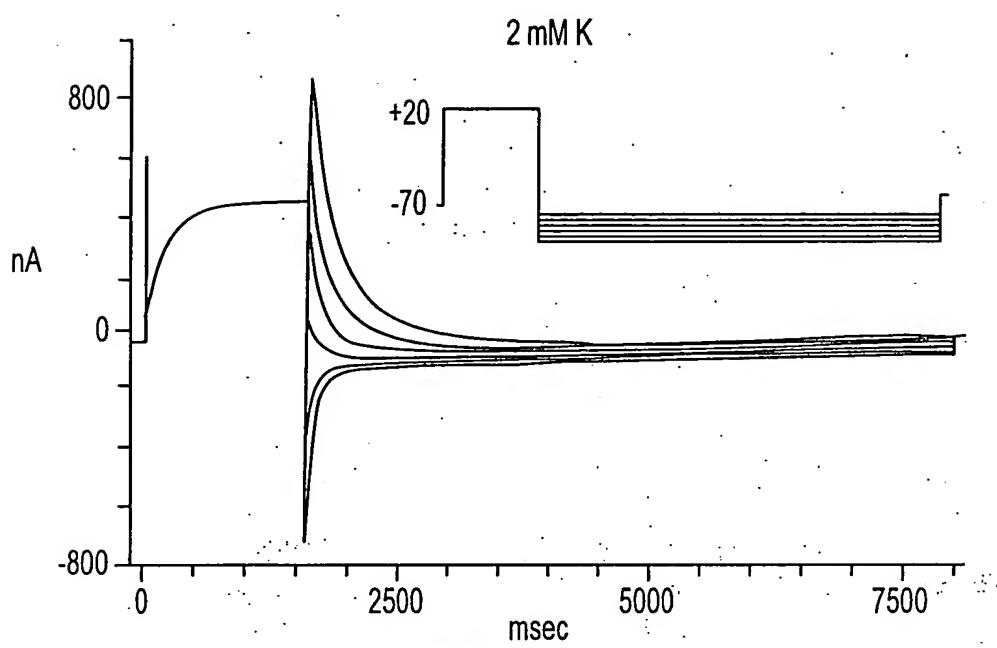


FIG. 3A

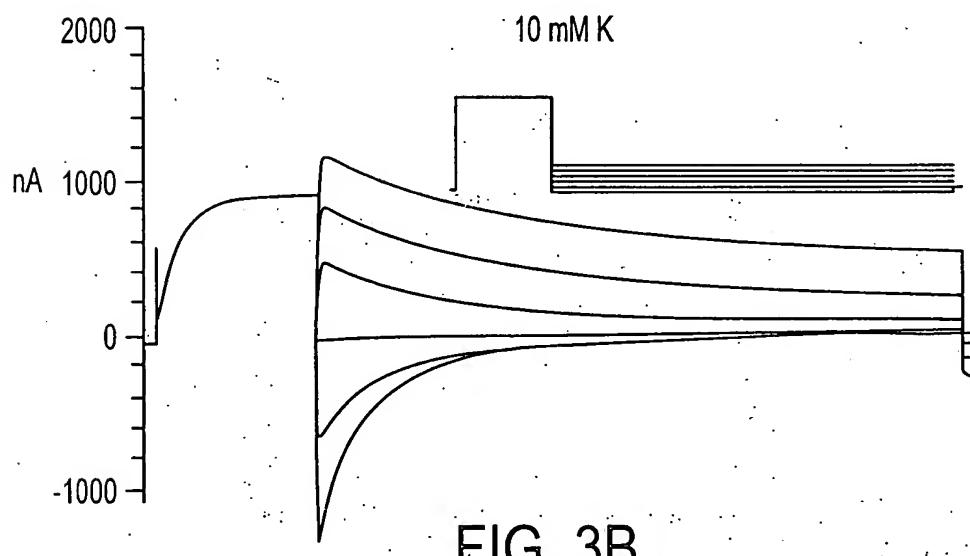


FIG. 3B

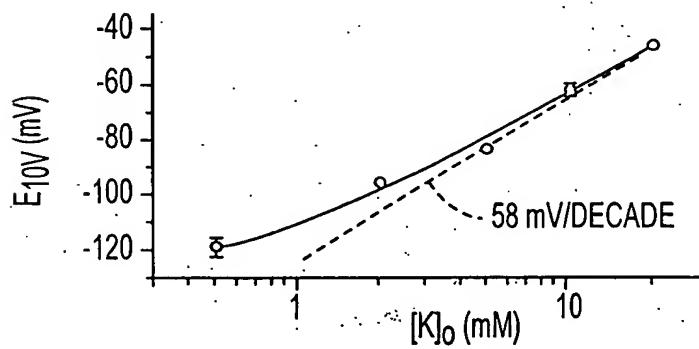


FIG. 3C

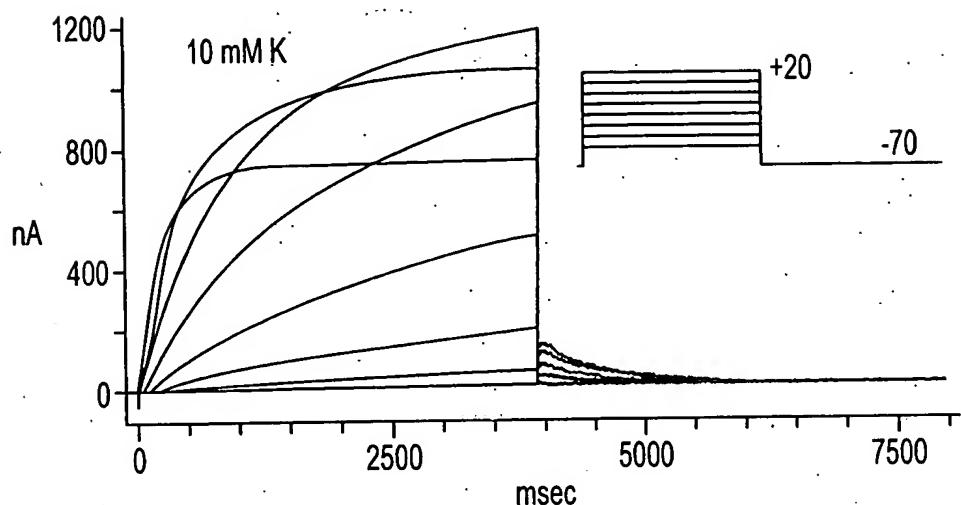


FIG. 4A

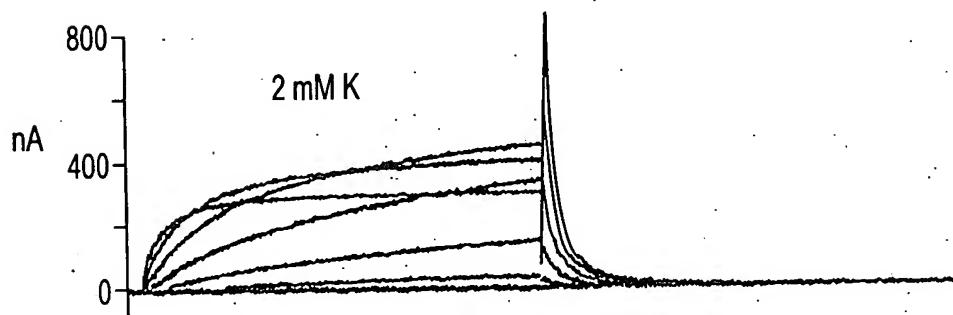


FIG. 4B

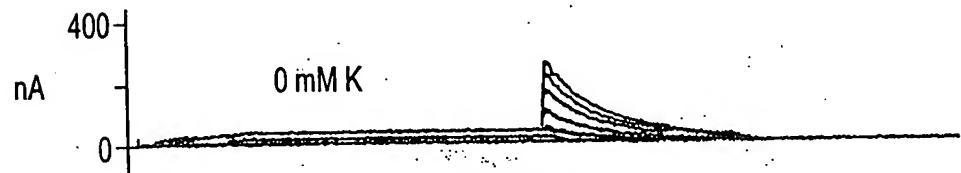


FIG. 4C

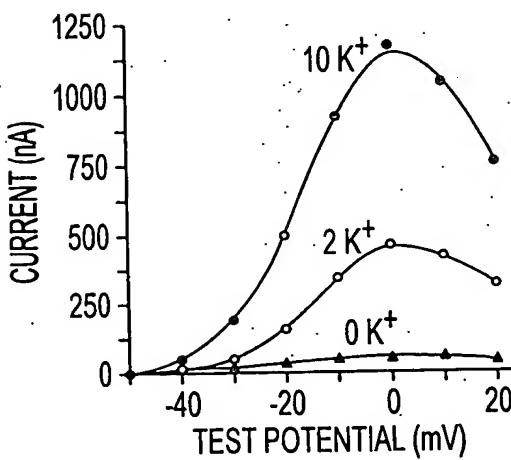


FIG. 4D

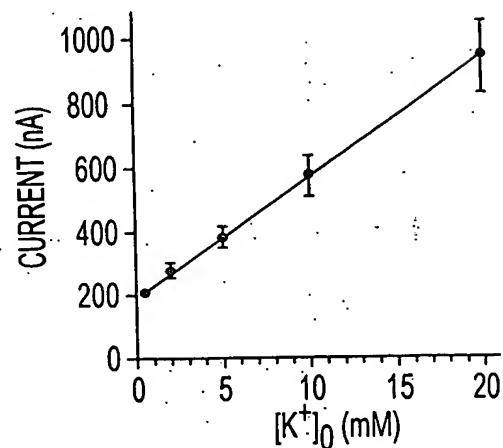


FIG. 4E

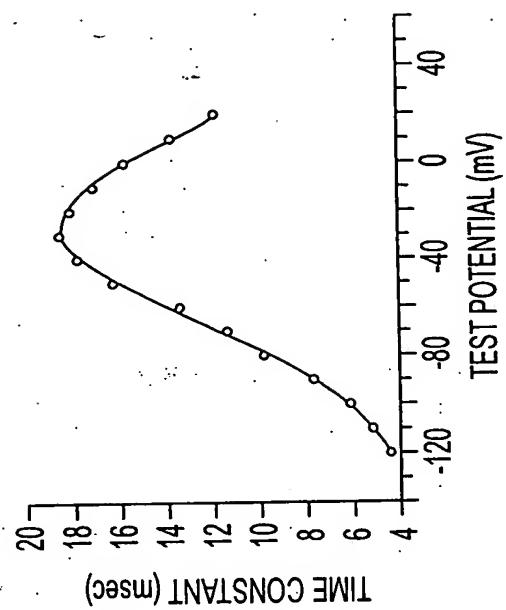


FIG. 5B

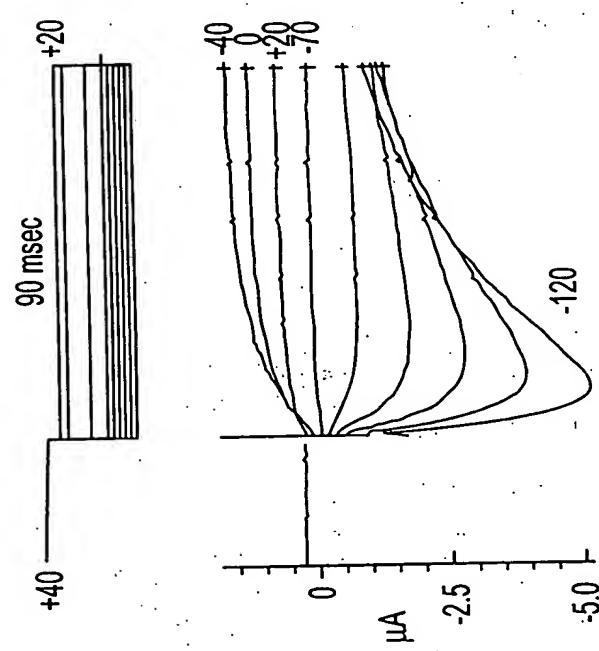


FIG. 5A

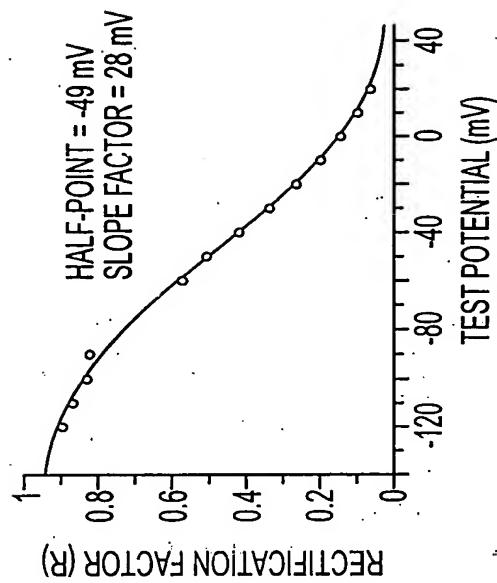


FIG. 5D

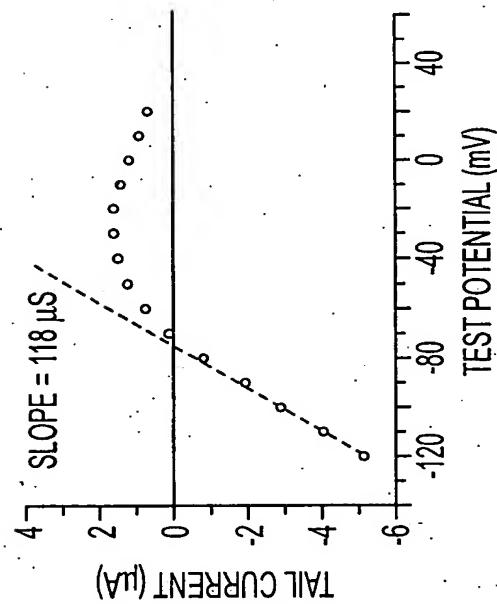


FIG. 5C

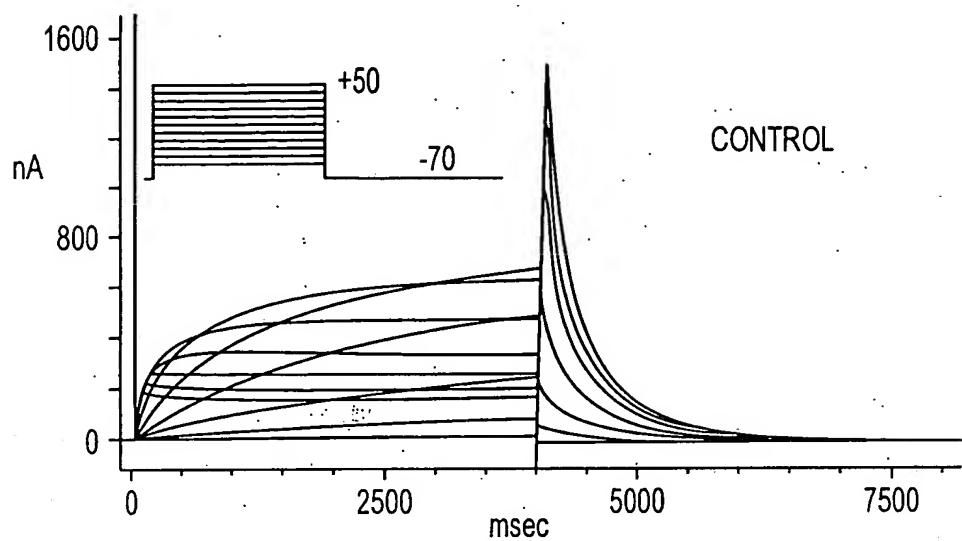


FIG. 6A

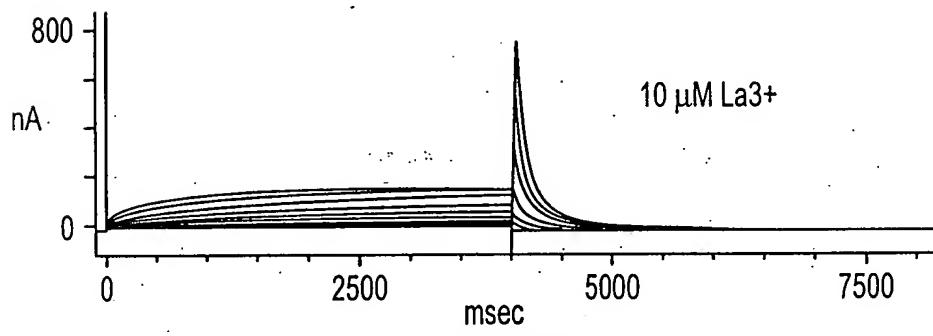


FIG. 6B

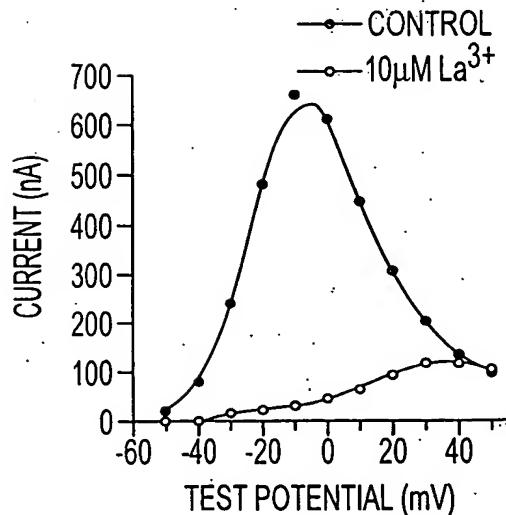


FIG. 6C

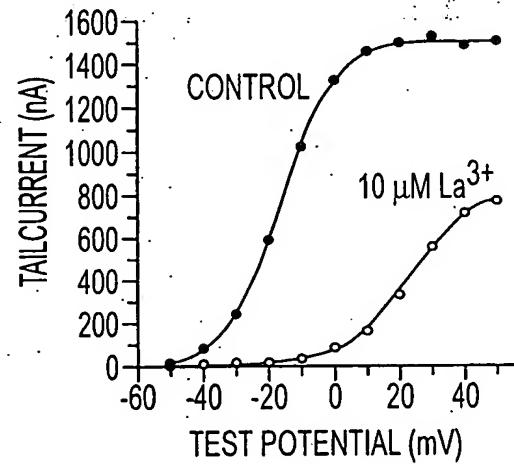


FIG. 6D

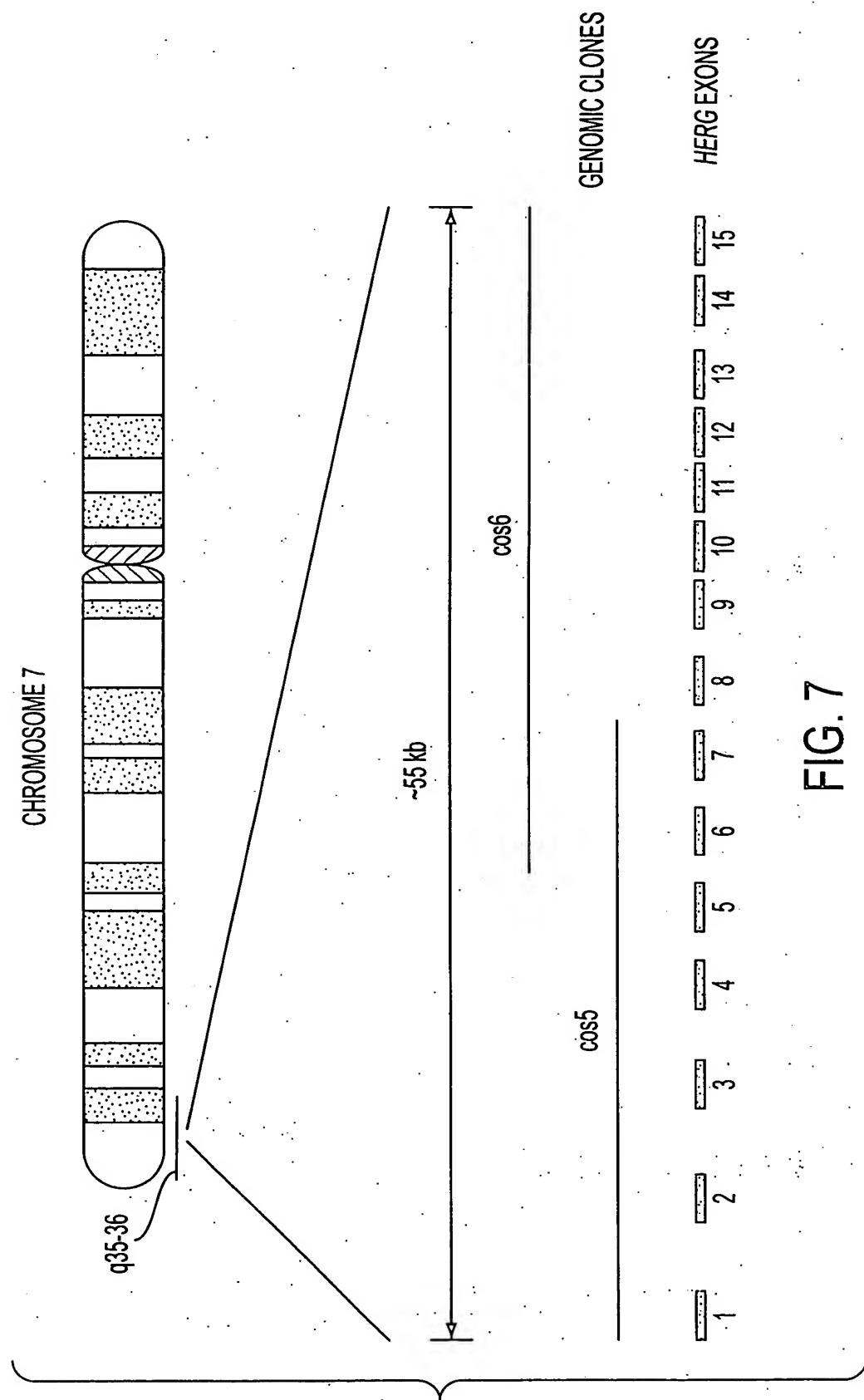


FIG. 7

AGCCTAGTGTGGGCCGGGCGGGCGGGTGGGTGGGGCCCGCCGCCATGGCTCAGGATGCCGTGGAGG-81
 ▽ M P V R R -55
 GGCCACGTGCGCCGCAGAACACCTTCTGGACACCATCATCCGCAAGTTGAGGGCCAGAGCCGTAAGTCATCATGCC-162
 G H V A P Q N T F L D T I I R K F E G O S R K F I I A -32
 AACGCTGGGTGGAGAACTGCGCCGTCACTACTGCAACGACGGCTCTGCAGCTGTGCGGCTACTCGCGGCCGAGGTG-243
 N A R V E N C A V I Y C N D G F C E L C G Y S R A E V -59
 ATGCAGCGACCCCTGCACCTGCGACTTCTGCACGGGCCGCGCACGCAGCGCCGCGCTGCCGCGCAGATCGCGCAGGCACTG-324
 M Q R P C T C D F L H G P R T Q R R A A A Q I A Q A L -86
 ▽
 CTGGGCAGGAGCGCAAAGTGGAAATGCCCTCTACCGAAAGATGGAGCTGCTTCTATGTCGGATGTGGT-405
 L G A E E R K V E I A F Y R K D G S C F L C L V D V V -113
 CCCGTGAAGAACGAGGATGGGCTGTCATGTCATCCTCAATTGAGGTGGTATGGAGAACGGACATGGTGGGTCC-486
 P V K N E D G A V I M F I L N F E V V M E K D M V G S -140
 ▽
 CCGGCTCATGACACCAACCACGGGCCCCCCCCACAGCTGGCTGGCCCAAGACCTCCGCCGAAGCTG-567
 P A H D T N H R G P P T S W L A P G R A K T F R L K L -167
 CCCGCGCTGGCGCTGACGGCCGGGAGTCGTCGGTGGCTGGCCGGCGGGCGGGCGCCCCGGCG-648
 P A L L A L T A R E S S V R S G G A G G A G A P G A V -194
 GTGGTGGACGTTGGACCTGACGCCGCGCACCCAGCAGCGAGTCGCTGGCCCTGGACGAAGTGACAGCCATGGACAACCAC-729
 V V D V D L T P A A P S S E S L A L D E V T A M D N H -221
 GTGCCAGGGCTCGGCCCCCGAGGAGCGCTGGTGGGTCCCGGCTCTCCGCCCGCAGCGCCGGCAGCTC-810
 V A G L G P A E E R R A L V G P G S P P R S A P G O L -248
 CCATGCCCGGGCGCACAGCCTCAACCCGACGCCCTCGGCTCAGCTGCAGCCTGGCCGGACGCGCTCCCGAGAACAGC-891
 P S P R A H S L N P D A S G S S C S L A R T R S R E S -275
 TGCGCCAGCGTGCGCCCGCCTCGTGGCCGACATCGAGGCCATGCCGCCGGGTGCTGCCCGCCACCGGCCAC-972
 C A S V R R A S S A D D I E A M R A G V L P P P P R H -302
 ▽
 GCCAGCACGGGGCCATGCACCCACTGCGCAGCGGCTTGCTCAACTCCACCTCGGACTCCGACCTCGTGCCTACCGCACC-1053
 A S T G A M H P L R S G L L N S T S D S D L V R Y R T -329
 ATTAGCAAGATTCCCCAAATCACCTCAACTTGTGGACCTCAAGGGCGACCCCTTCTGGCTCGCCACCAGTGACCGT-1134
 I S K I P Q I T L N F V D L K G D P F L A S P T S D R -356
 ▽
 GAGATCATAGCACCTAACGATAAAGGAGCGAACCCACAATGTCAGTGAGAGGTACCCAGGTCTGTCCTGGGCGCACC-1215
 E I I A P K I K E R T H N V T E K V T O V L S L G A D -383
 GTGCTGCCCTGAGTACAAGCTGAGGACCGCAGCGCATCCACCGCTGGACCATCTGCATTACAGCCCTCAAGGCCGTGTGG-1296
 V L P E Y K L Q A P R I H R W T I L H Y S P F K A V W -410
 ▽
 GACTGGCTCATCCTGCTGCTGGTCATCTACACGGCTGCTTCACACCCACTCGGCTGCCCTCTGCTGAAGGAGACGGAA-1377
 D W L I L L V I Y T A V F T P Y S A A F L L K E T E -437
 S1
 GAAGGCCGCGCTGCTACCGAGTGTGGCTACGCCGCGCTGGCTGTGGACCTCATCGTGGACATCATGTCATT-1458
 E G P P A T E C G Y A C Q P L A V V D L I V D I M F I -464
 S2
 GTGGACATCCTCATCAACTCCGACCACTACGTCAATGCCAACGAGGAGGTGGCAGCCACCCGGCCATGCCGTC-1539
 V D I L I N F R T T Y V N A N E E V V S H P G R I A V -491
 ▽
 CACTACTCAAGGGCTGGTCATCGACATGGTGCCGCATCCCTCGACCTGCTCATCTCGGCTCTGGCTCTGAG-1620
 H Y F K G W F L I D M V A A I P F D L L I F G S G S E -518
 S3
 GAGCTGATCGGGCTGCTGAAGACTGCGCGCTGCTGGCTGGTGCCTGGCGGAAGCTGGATGCTACTCAGAGTAC-1701
 E L I G L L K T A R L L R L V R V A R K L D R Y S E Y -545
 S4
 GGCAGGCCGTGCTGCTCATGTGCACCTTGCGCTACCGCAGCTGGCTAGCCTGCATGGTACGCCATGGC-1782
 G A A V L F L L M C T F A L I A H W L A C I W Y A I G -572
 S5
 AACATGGAGCAGCCACACATGGACTCACGCATGGCTGGCTGCACAAACCTGGCGACCAAGATAGGCAAACCTACAACAGC-1863
 N M E O P H M D S R I G W L H N L G D O I G K P Y N S -599
 AGCGGCTGGCGGCCCTCCATCAAGGACAAGTATGTGACGGCGCTACTTCACCTCAGCAGCCTCACCAAGTGTGGC-1944
 S G L G G P S I K D K Y V T A L Y F T F S S L T S V G -626
 Pore ▽
 TTGGCAACGTCTCCAACACCAACTCAGAGAAGATCTCTCCATCTGCGCTATGCTCATGGCTCCCTCATGTATGCT-2025
 F G N V S P N T N S E K I F S I C V M L I G S L M Y A -653
 S6

AGCATCTCGGCAACGTGTCGCCATCATCCAGCGGTGACTCGGGCACAGCCCGTACCAACACAGATGCTGCGGGTG-2106
 S I F G N V S A I I O R L Y S G T A R Y H T Q M L R V -680

CGGGAGTTCATCCGCTTCCACAGATCCCCAATCCCTGCGCCAGCGCCTCGAGGAGTACTTCAGCACGCCCTGGTCTAC-2187
 R E F I R F H Q I P N P L R Q R L E E Y F Q H A W S Y -707
 ▽
 ACCAACGGCATCGACATGAACCGCGGTGCTGAAGGGCTTCCCTGAGTGCCTGCAGGCTGACATCTGCCCTGCACCTGAACCGC-2268
 T N G I D M N A V L K G F P E C L Q A D I C L H L N R -734
 TCACTGCTGCAGCACTGCAAACCCCTTCCGAGGGCCACCAAGGGCTGCCCTGGGCCATGAAGTTCAAGACCACA-2349
 S L L Q H C K P F R G A T K G C L R A L A M K F K T T -761
 CATGCACCGCCAGGGGACACACTGGTGCATGCTGGGACCTGCTACCCGCCCTGTACTTCATCTCCGGGCTCCATCGAG-2430
 H A P P G D T L V H A G D L L T A L Y F I S R G S I E -788
 ▽
 ATCCTGCGGGGCGACGTCGTGGCCATCCTGGGAGAATGACATCTTGGGAGCCTCTGAACCTGTATGCAAGGCCT-2511
 I L R G D V V V A I L G K N D I F G E P L N L Y A R P -815
 cNBD
 GGCAAGTCGAACGGGGATGTGGCCCTCACCTACTGTGACCTACACAAGATCCATGGGACGACCTGCTGGAGGTGCTG-2592
 G K S N G D V R A L T Y C D L H K I H R D D L L E V L -842
 ▽
 GACATGTACCCCTGAGTTCTCCGACCACTTCTGGTCCAGCCTGGAGATCACCTCAACCTGCGAGATACCAACATGATCCCG-2673
 D M Y P E F S D H F W S S L E I T F N L R D T N M I P -869
 GGCTCCCCGGCAGTACGGAGTTAGAGGGTGGCTTCAGTGGCAACGCAAGCGCAAGTTGCTCTCCGAGGCCACGGAC-2754
 G S P G S T E L E G G F S R Q R K R K L S F R R R T D -896
 ▽
 AAGGACACGGAGCAGCCAGGGAGGTGTCGGCTTGGGCGGGCGGGGGCAGGGCCGAGTAGCCGGGGCGGGCG-2835
 K D T E Q P G E V S A L G P G R A G A G P S S R G R P -923
 GGGGGGGCGTGGGGGAGAGCCCGTCCAGTGGCCCCCTCCAGGCCCTGAGAGCAGTGAGGATGAGGGCCAGGCCAGCTCC-2916
 G G P W G E S P S S G P S S P E S S E D E G P G R S S -950
 AGCCCCCTCCGCTGGTGCCTCTCCAGCCCCAGGGCCCCGGAGAGGCCGGGTGGGAGGCCCTGATGGAGGGACTGC-2997
 S P L R L V P F S S P R P P G E P P G G E P L M E D C -977
 ▽
 GAGAAGAGCAGCGACACTTCAACCCCTGTCAGGCCCTCTCAGGAGTGTCCAACATTTCAGCTCTGGGGGACAGT-3078
 E K S S D T C N P L S G A F S G V S N I F S F W G D S -1004
 CGGGGCCGCACTTACAGGAGCTCCCTCGATGCCCGCCCCACCCCCAGGCCCTCAACATCCCCCTCTCCAGCCGGT-3159
 R G R Q Y Q E L P R C P A P T P S L L N I P L S S P G -1031
 ▽
 CGGGCCCCCGGGCGACGTGGAGAGCAGGCTGGATGCCCTCCAGGCCAGCTAACAGGCTGGAGACCCGGCTAGTGCA-3240
 R R P R G D V E S R L D A L Q R Q L N R L E T R L S A -1058
 GACATGCCACTGTCTGCGAGTACAGAGGCAGATGACGCTGGCCGCCCTACAGTGCTGACCCGGGG-3321
 D M A T V L Q L L Q R Q M T L V P P A Y S A V T T P G -1085
 ▽
 CCTGGCCCCACTTCCACATCCCGCTGTTGCCGTAGCCCCCTCCCCACCCCTCACCTGGACTCGCTTCTCAGGTTCC-3402
 P G P T S T S P L L P V S P L P T L T L D S L S Q V S -1112
 CAGTTCATGGCGTGTGAGGAGCTGCCCGGGGGCCAGAGCTCCCCAAGAAGGCCACACGACGCCCTCCCTACCG-3483
 Q F M A C E E L P P G A P E L P Q E G P T R R L S L P -1139
 GGCCAGCTGGGGGCCCTCACCTCCAGCCCCCTGCACAGACACGGCTGGACCCGGCAGTTAGTGGGCTGCCAGTGTGG-3564
 G Q L G A L T S Q P L H R G S D P G S * -1159
 ACACGTGGCTCACCAAGGATCAAGGCCTGCTGGGGCGCTCCCTTGGAGGGCCCTGCTCAGGAGGCCCTGACCGTGGAG-3645
 GGGAGAGGAACCTGAAAGCACAGCTCCTCCCCCAGCCCTGGGACCATCTTCTCCCTGAGTCCCTGGGCCAGTGAGAG-3726
 GGGCAGGGCAGGGCCGGCAGTAGGTGGGGCTGTGGTCCCCACTGCCCTGAGGGCATTAGTGGCTAACTGCCCGA-3807
 GGCACCCGGCCCTGGGCCTTAGGCACCTCAAGGACTTTCTGCTATTACTGCTCTTATTGTTAAGGATAATAATTAAAGGA-3888
 TCATATGAATAATTAAATGAAGATGCTGATGACTATGAATAATAATTATCCTGAGGAG (A)n -3949

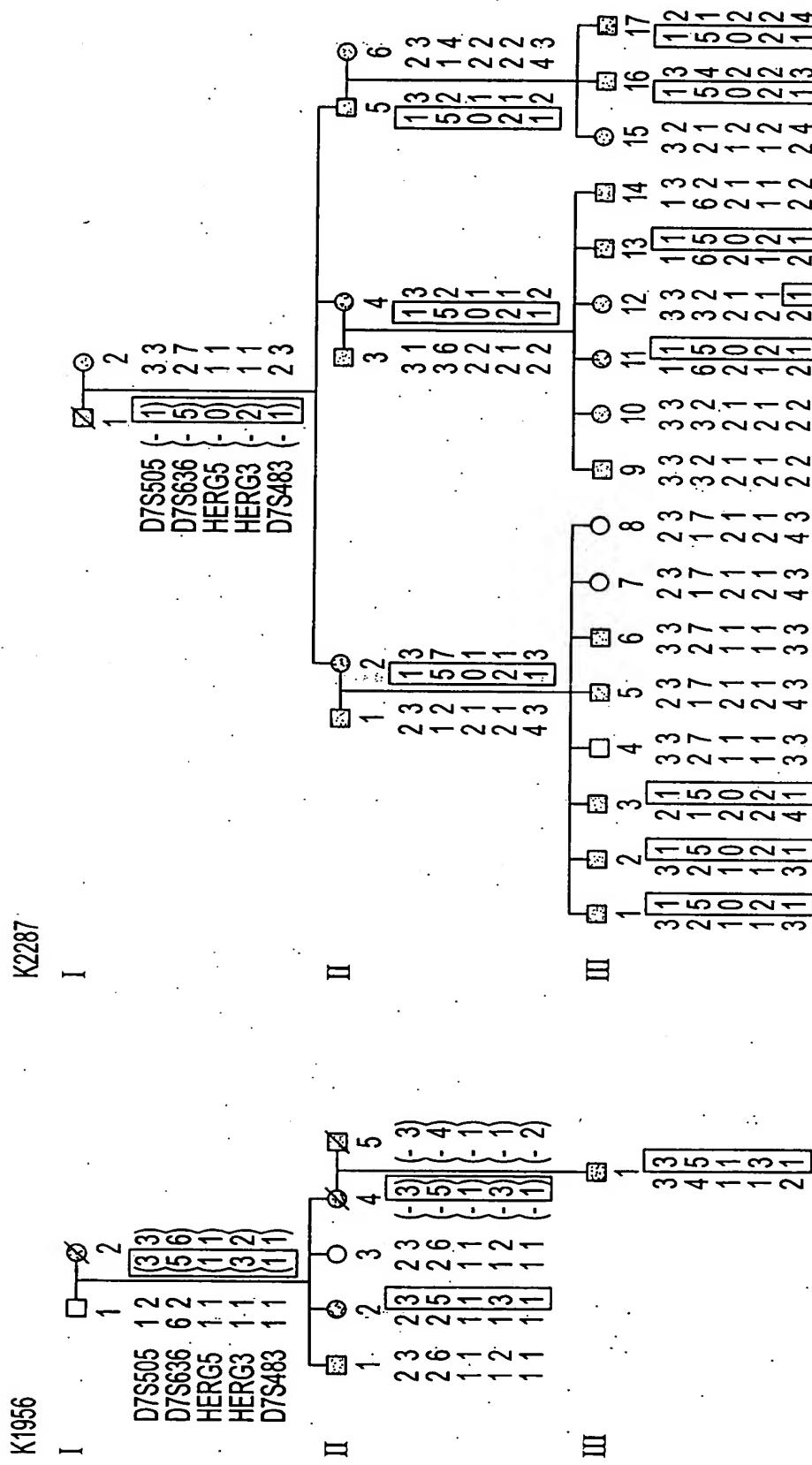


FIG. 9A

FIG. 9B

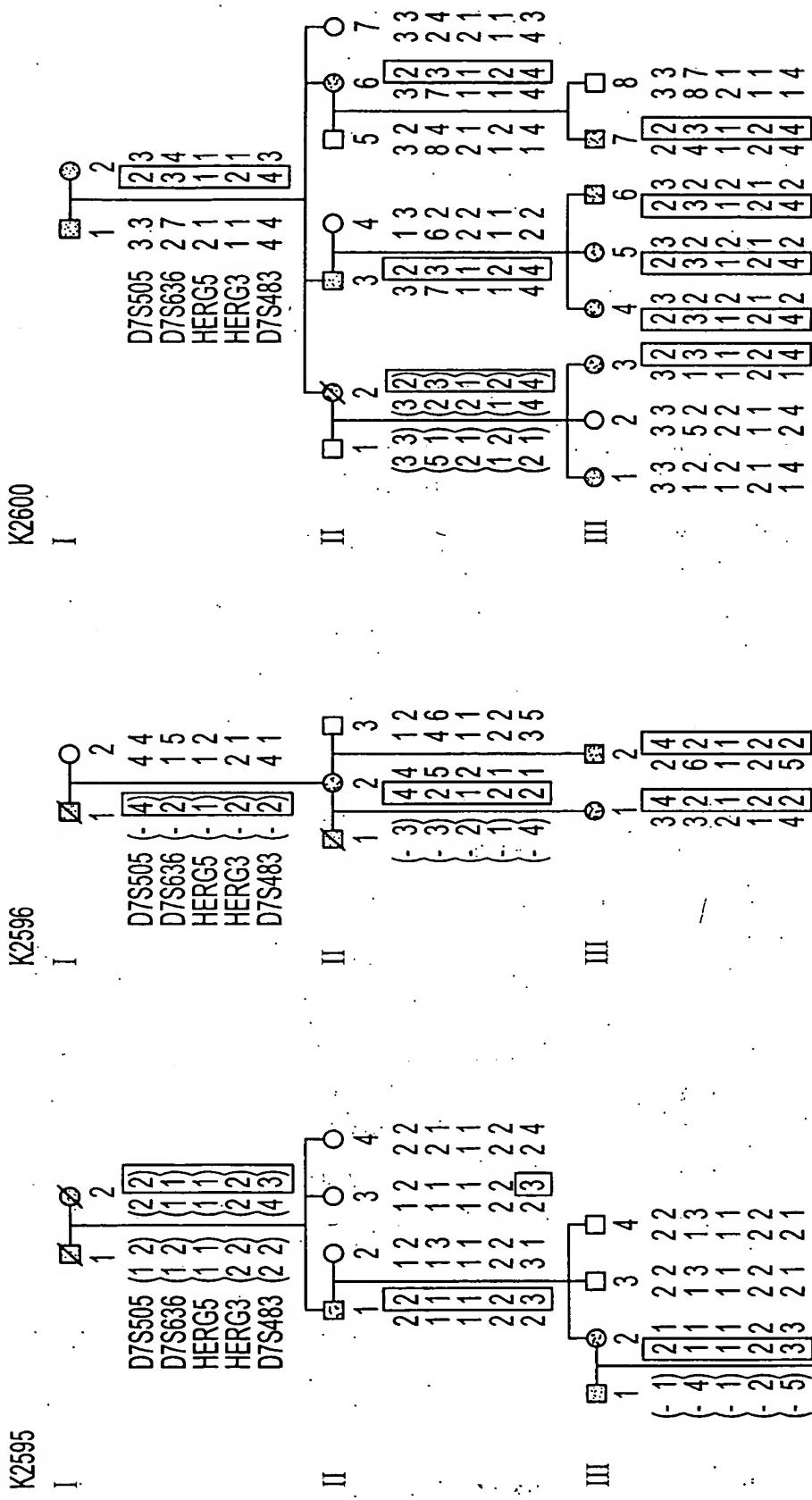


FIG. 9E

FIG. 9D

FIG. 9C

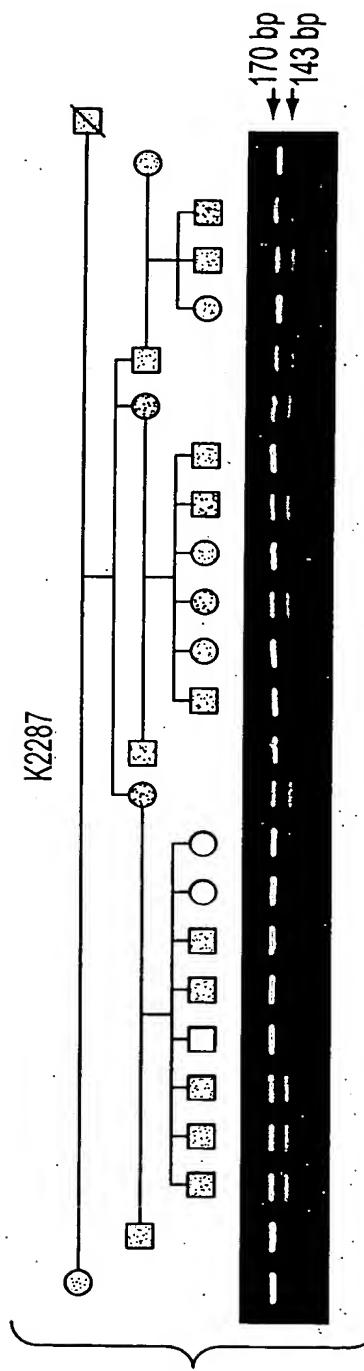


FIG. 10A

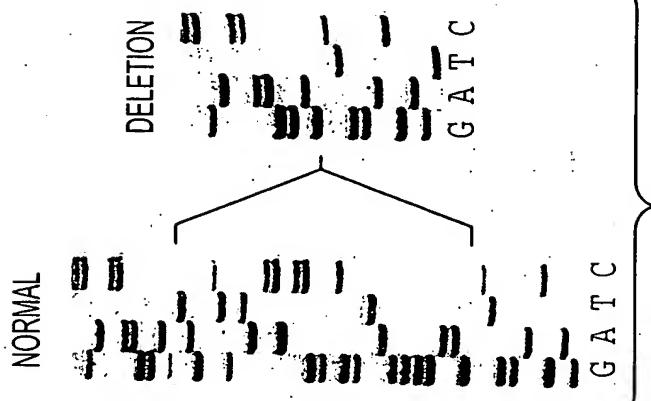


FIG. 10B

TGG TTC CTC [ATC GAC ATG GTG GCC ATC CCC TTC] GAC CTG CTC SEQ ID NO:96
W F L I D M V A A I P F D L L SEQ ID NO:97
SEQ ID NO:97

SS3

↓

FIG. 10C

NORMAL GTC ATC TAC ACG GCT GTC TTC ACA CCC TAC TCG GCT GCC TTC CTG CTG AAG GAG SEQ ID NO:98
V I Y T A V F T P Y S A A F L L K E SEQ ID NO:99
DELETION GTC ATC TAC [CGG CTG TCT TCA CAC CCT ACT CGG CTG CCT TCC TGC TGA]
V I Y R L S S H P T R L P S C SEQ ID NO:100
SEQ ID NO:101

FIG. 11C

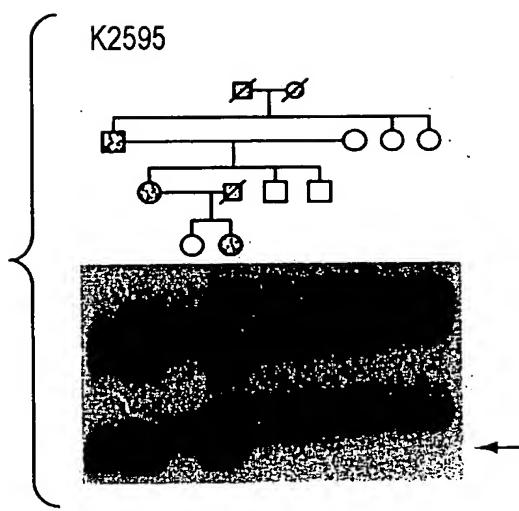


FIG. 11A

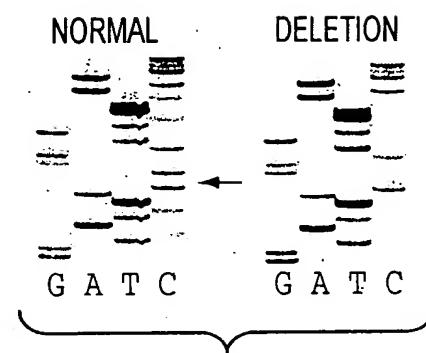


FIG. 11B

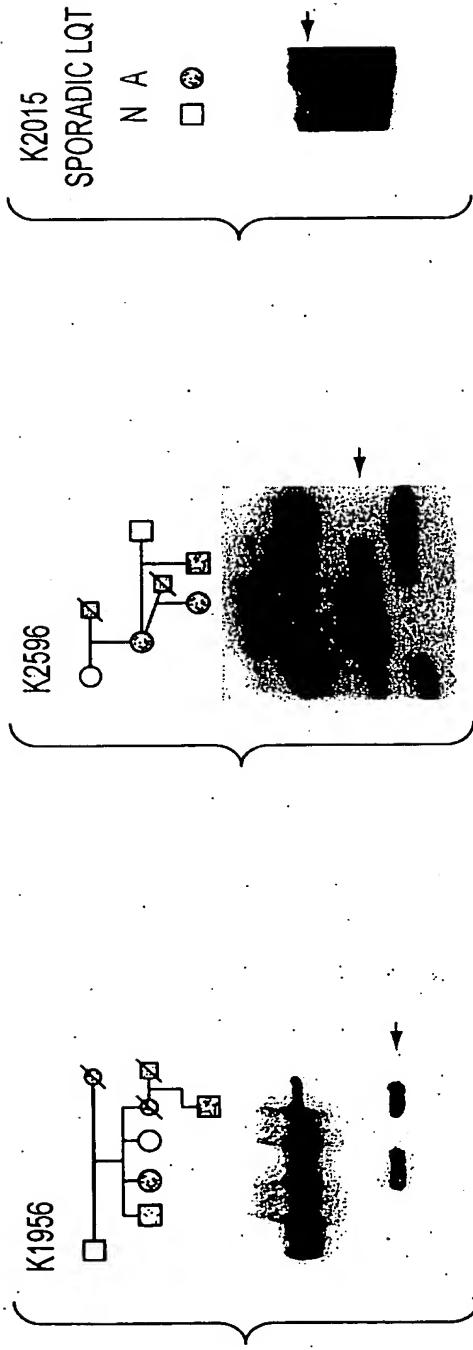


FIG. 12E

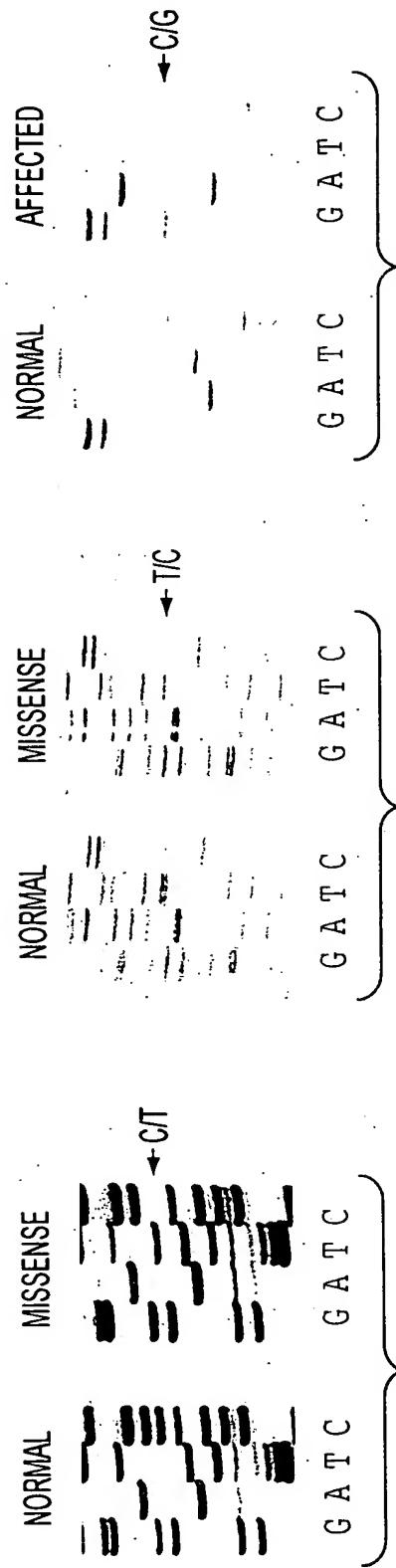


FIG. 12E

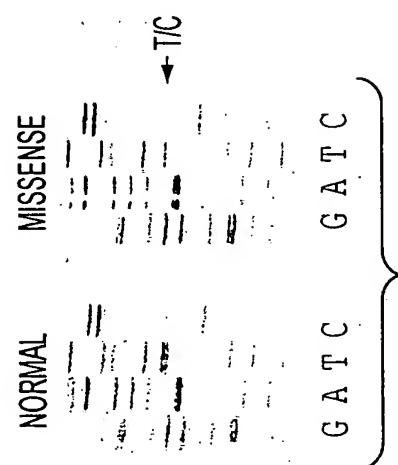
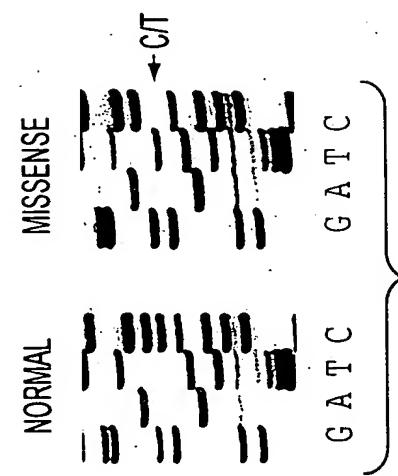


FIG. 12D



EIG 12B

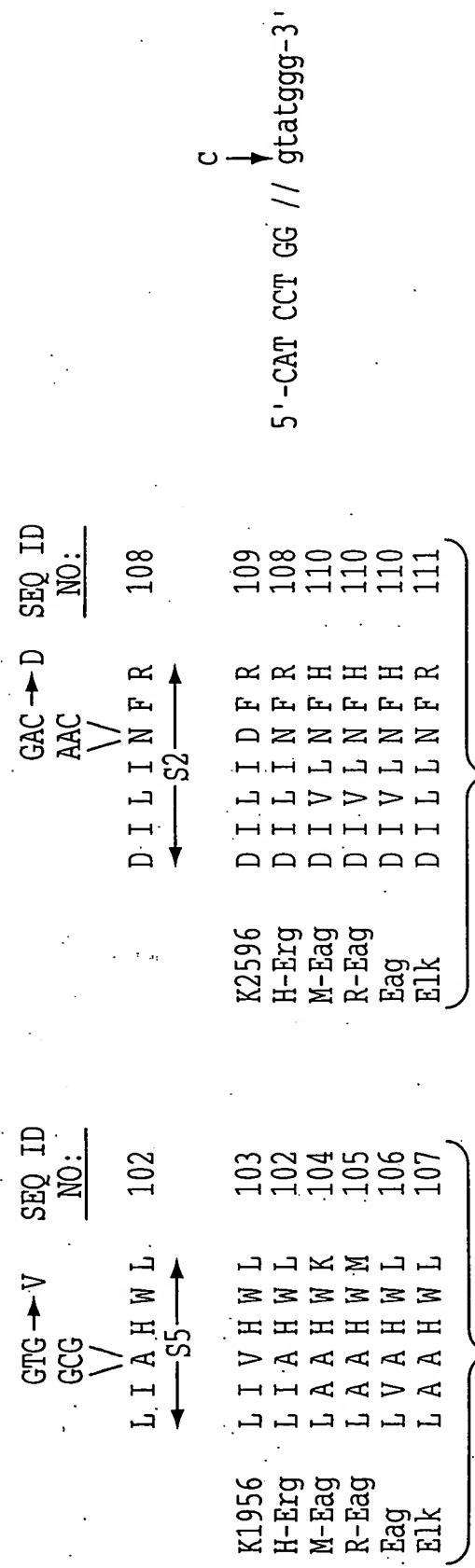


FIG. 12G

FIG. 12H

FIG. 12I



FIG. 13A

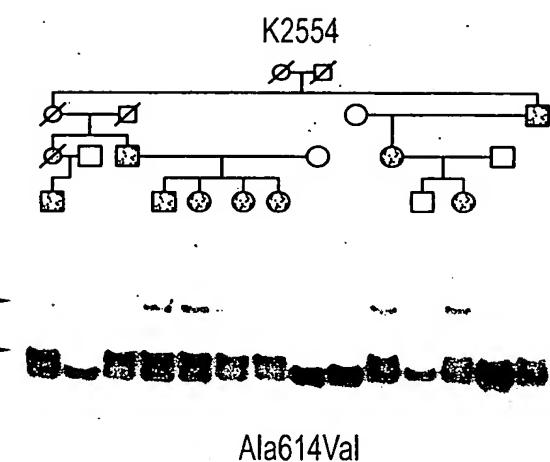


FIG. 13B

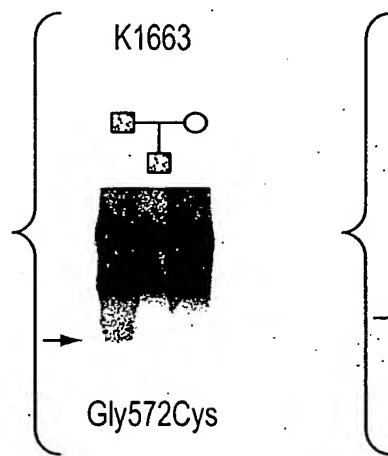


FIG. 13C

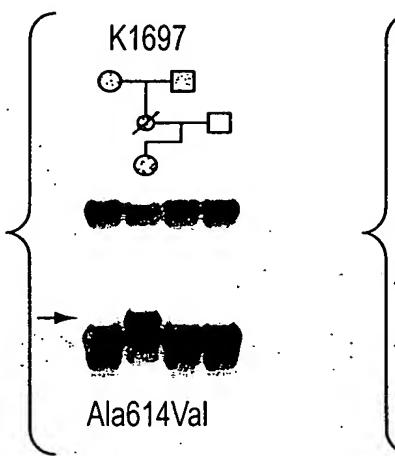


FIG. 13D

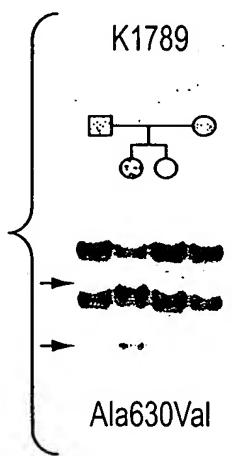


FIG. 13E

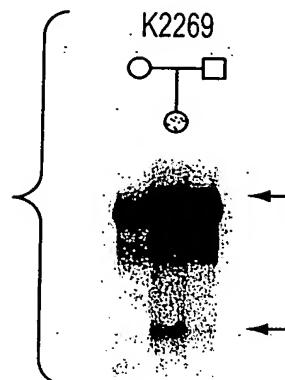


FIG. 14A

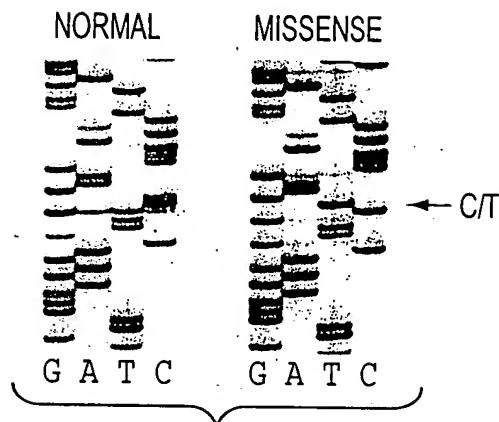


FIG. 14B

A sequence alignment diagram at the top shows 'AGC → S' and 'GGC' with a vertical line between them. Below is a sequence 'S V G F G N V S' with a bracket labeled 'PORE' underneath. To the right is 'SEQ ID NO: 112'.

K2269	S V G F S N V S	113
H-Erg	S V G F G N V S	112
M-Eag	S V G F G N I A	114
R-Eag	S V G F G N I A	114
Eag	S V G F G N V A	115
Elk	S V G F G N V S	112
Shaker	T V G Y G D M T	116

FIG. 14C

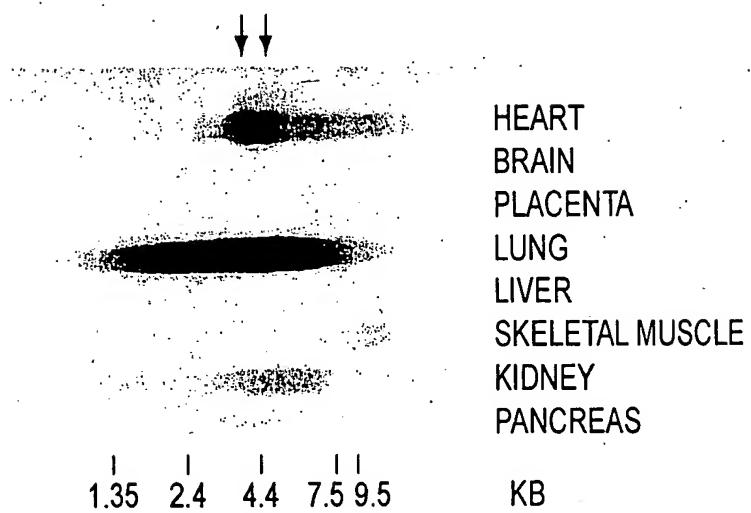


FIG. 15